

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/987, 151 D
Source: IFW16
Date Processed by STIC: 08/22/2005

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 08/22/2005

PATENT APPLICATION: US/09/981,151D

TIME: 10:02:32

Input Set : D:\Cura 468 SEQ list 0705.txt

Output Set: N:\CRF4\08222005\I981151D.raw

(pg.6)

3 <110> APPLICANT: Guo, Xiaojia
 5 <120> TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
 7 <130> FILE REFERENCE: 21402-168
 9 <140> CURRENT APPLICATION NUMBER: 09/981,151D
 10 <141> CURRENT FILING DATE: 2001-10-16
 12 <150> PRIOR APPLICATION NUMBER: 60/241,040
 13 <151> PRIOR FILING DATE: 2000-10-17
 15 <150> PRIOR APPLICATION NUMBER: 60/241,058
 16 <151> PRIOR FILING DATE: 2000-10-17
 18 <150> PRIOR APPLICATION NUMBER: 60/241,063
 19 <151> PRIOR FILING DATE: 2000-10-17
 21 <150> PRIOR APPLICATION NUMBER: 60/241,243
 22 <151> PRIOR FILING DATE: 2000-10-17
 24 <150> PRIOR APPLICATION NUMBER: 60/242,152
 25 <151> PRIOR FILING DATE: 2000-10-20
 27 <150> PRIOR APPLICATION NUMBER: 60/242,482
 28 <151> PRIOR FILING DATE: 2000-10-23
 30 <150> PRIOR APPLICATION NUMBER: 60/242,611
 31 <151> PRIOR FILING DATE: 2000-10-23
 33 <150> PRIOR APPLICATION NUMBER: 60/242,612
 34 <151> PRIOR FILING DATE: 2000-10-23
 36 <150> PRIOR APPLICATION NUMBER: 60/242,880
 37 <151> PRIOR FILING DATE: 2000-10-24
 39 <150> PRIOR APPLICATION NUMBER: 60/242,881
 40 <151> PRIOR FILING DATE: 2000-10-24
 42 <150> PRIOR APPLICATION NUMBER: 60/259,028
 43 <151> PRIOR FILING DATE: 2000-12-29
 45 <150> PRIOR APPLICATION NUMBER: 60/269,813
 46 <151> PRIOR FILING DATE: 2001-02-20
 48 <150> PRIOR APPLICATION NUMBER: 60/286,324
 49 <151> PRIOR FILING DATE: 2001-04-25
 51 <150> PRIOR APPLICATION NUMBER: 60/294,108
 52 <151> PRIOR FILING DATE: 2001-05-29
 54 <150> PRIOR APPLICATION NUMBER: 60/303,968
 55 <151> PRIOR FILING DATE: 2001-07-09
 57 <160> NUMBER OF SEQ ID NOS: 166
 59 <170> SOFTWARE: PatentIn Ver. 2.1
 61 <210> SEQ ID NO: 1
 62 <211> LENGTH: 2997
 63 <212> TYPE: DNA
 64 <213> ORGANISM: Homo sapiens
 66 <220> FEATURE:
 67 <221> NAME/KEY: misc_feature

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68 <222> LOCATION: (857)..(858)

69 <223> OTHER INFORMATION: Wherein n is an a or t or c or g.

71 <220> FEATURE:

72 <221> NAME/KEY: misc_feature

73 <222> LOCATION: (2383)

74 <223> OTHER INFORMATION: Wherein n is an a or t or c or g.

76 <220> FEATURE:

77 <221> NAME/KEY: misc_feature

78 <222> LOCATION: (2983)

79 <223> OTHER INFORMATION: wherein n is an a or t or c or g.

81 <400> SEQUENCE: 1

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83 ttggcgcagg tggccgagca ggtgagtccc gggcgctccc accagcgcgg aaaccgcggg 120

84 tccggacagc tggaggcgag tccccgcgg ctcctctccc gcggaccccc cgtctcacc 180

85 gcgatgtcgc cgctgttttc cgcaggcacc tgcgtgcgcc atgggacccg cagcggcagc 240

86 gcctgggagc ccgagcgtcc cgcgtcctcc tccaccgcgg gagcggccgg gctggatgga 300

87 aaagggcggg acatggatga agctggaaac catcgttctc agcaaactaa cacaggaaca 360

88 gaaaaccaa cactgcatgt tctcactcaa tatgacctgg tctctgccta cgaggttgac 420

89 cacaggggagc attacgtgtc ccatgaaatc atgcaccatc agcggcggag aagagcagtg 480

90 gccgtgtccg aggttgagtc tcttcacctt cggctgaaag gccccaggca cgacttccac 540

91 atggatctga ggacttccag cagcctagtg gctcctggct ttattgtgca gacgttggga 600

92 aagacaggca ctaagtctgt gcagacttta ccgccagagg acttctgttt ctatcaaggc 660

93 tctttgcatg cacacagaaa ctgccatcg catggaggga agttctgtga gggctccact 720

94 cgcactctga agctctgcaa cagtcagaaa tgtccccggg acagtgttga cttccgtgct 780

95 gctcagtgtg ccgagcacia cagcagacga ttcagagggc ggcactacia gtggaagcct 840

W--> 96 **tacactcaag tagaagnnga cttatgcaaa ctctactgta tcgcagaagg atttgatttc 900**

97 ttcttttctt tgtcaaataa agtcaaagat gggactccat gctcggagga tagccgtaat 960

98 gtttgatag atgggatatg tgagctcagt gtggtgtcca catctgcgca catgccccag 1020

99 cctcccaagg aagacctctt catcttgcca gatgagtata agtcttgctt acggcataag 1080

100 cgctctcttc tgaggtecca tagaaatgaa gaactgaacg tggagacctt ggtggtggtc 1140

101 gacaaaaaga tgatgcaaaa ccatggccat gaaaatatca ccacctacgt gctcacgata 1200

102 ctcaacatgg tatctgcttt attcaaagat ggaacaatag gaggaacat caacattgca 1260

103 attgtaggtc tgattcttct agaagatgaa cagccaggac tggtgataag tcaccacgca 1320

104 gaccacacct taagtagctt ctgccagtgg cagtctggat tgatggggaa agatgggact 1380

105 cgtcatgacc acgccatctt actgactggc ctggatatat gttcctggaa gaatgagccc 1440

106 tgtgacactt tgggatttgc acccataagt ggaatgtgta gtaaatatcg cagctgcacg 1500

107 attaatagag atacaggtct tggactggcc ttcaccattg cccatgagtc tggacacaac 1560

108 tttggcatga ttcattgatg agaagggaac atgtgtaaaa agtccgaggg caacatcatg 1620

109 tcccctacat tggcaggacg caatggagtc ttctcctggc caccctgcag ccgccagtat 1680

110 ctacacaaat ttctaagcac cgctcaagct atctgccttg ctgatcagcc aaagcctgtg 1740

111 aaggaataca agtatcctga gaaattgcca ggagaattat atgatgcaaa cacacagtgc 1800

112 aagtggcagt tcggagagaa agccaagctc tgcagtctgg actttaaaaa ggacatctgt 1860

113 aaagccctgt ggtgccatcg tattggaagg aaatgtgaga ctaaatttat gccagcagca 1920

114 gaaggcacia tttgtgggca tgacatgtgg tgccggggag gacagtgtgt gaaatatggt 1980

115 gatgaaggcc ccaagcccac ccatggccac tggtcggact ggtcttcttg gtcccatgc 2040

116 tccaggacct gcggaggggg agtatctcat aggagtcgcc tctgcaccaa ccccaatcca 2100

117 tcgcatggag ggaagtcttg tgagggtccc actcgcactc tgaagctctg caacagtcag 2160

118 aaatgtcccc gggacagtgt tgacttccgt gctgctcagt gtgccgagca caacagcaga 2220

119 cgattcagag ggcggcacta caagtggaag cctcaggact tatgcaaact ctactgtatc 2280

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120 gcagaaggat ttgatttctt cttttctttg tcaaataaag tcaaagatgg gactccatgc 2340
121 tcggaggata gccgtaatgt ttgtatagat gggatatgtg agnttggatg tgacaatgtc 2400
122 cttggatctg atgctgttga agacgtctgt ggggtgtgta acgggaataa ctcagcctgc 2460
123 acgattcaca ggggtctcta caccaagcac caccacacca accattatca catggtcacc 2520
124 attccttctg gagcccgagg tatccgcata tatgaaatga acgtctctac ctcctacatt 2580
125 tctgtgcgca atgccctcag aaggctactac ctgaatgggc actggaccgt ggactggccc 2640
126 ggccgggtaca aattttcggg cactactttc gactacagac ggctcctataa tgagcccgag 2700
127 aacttaatcg ctactggacc aaccaacgag acactgattg tggagctgct gtttcagggg 2760
128 aggaaccggt gtgttgcttg ggaataactcc atgcctcgtt tggggaccga gaagcagccc 2820
129 cctgcccagc ccagctacac ttggggccatc gtgcgctctg agtgctccgt gtcctgcgga 2880
130 gggggtaggt gccttccagt gctgctcctg gaggcagcat gtcagccttc agccactgcg 2940
131 tacattgcac tggcctttct tgaatcctaa tgagcagccc ggnngcttct cctgcca 2997

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134 <210> SEQ ID NO: 2

135 <211> LENGTH: 986

136 <212> TYPE: PRT

137 <213> ORGANISM: Homo sapiens

139 <220> FEATURE:

140 <221> NAME/KEY: VARIANT

141 <222> LOCATION: (283)

142 <223> OTHER INFORMATION: Wherein Xaa is any amino acid.

144 <220> FEATURE:

145 <221> NAME/KEY: VARIANT

146 <222> LOCATION: (792)

147 <223> OTHER INFORMATION: Wherein Xaa is any amino acid.

149 <400> SEQUENCE: 2

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151   1           5           10           15
153 Leu Leu Ala Gln Val Ala Glu Gln Val Ser Pro Gly Arg Ser His Gln
154           20           25           30
156 Arg Gly Asn Arg Gly Ser Gly Gln Leu Glu Ala Ser Pro Pro Arg Leu
157           35           40           45
159 Leu Ser Arg Gly Pro Arg Arg Leu Thr Ala Met Ser Pro Leu Phe Ser
160           50           55           60
162 Ala Gly Thr Cys Val Arg His Gly Thr Arg Ser Gly Ser Ala Trp Glu
163   65           70           75           80
165 Pro Glu Arg Pro Ala Ser Ser Ser Thr Arg Gly Ala Ala Gly Leu Asp
166           85           90           95
168 Gly Lys Gly Arg Asp Met Asp Glu Ala Gly Asn His Arg Ser Gln Gln
169           100          105          110
171 Thr Asn Thr Gly Thr Glu Asn Gln Thr Leu His Val Leu Thr Gln Tyr
172           115          120          125
174 Asp Leu Val Ser Ala Tyr Glu Val Asp His Arg Gly Asp Tyr Val Ser
175           130          135          140
177 His Glu Ile Met His His Gln Arg Arg Arg Arg Ala Val Ala Val Ser
178 145           150          155          160
180 Glu Val Glu Ser Leu His Leu Arg Leu Lys Gly Pro Arg His Asp Phe
181           165          170          175
183 His Met Asp Leu Arg Thr Ser Ser Ser Leu Val Ala Pro Gly Phe Ile
184           180          185          190

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186 Val Gln Thr Leu Gly Lys Thr Gly Thr Lys Ser Val Gln Thr Leu Pro
187      195      200      205
189 Pro Glu Asp Phe Cys Phe Tyr Gln Gly Ser Leu Arg Ser His Arg Asn
190      210      215      220
192 Ser Pro Ser His Gly Gly Lys Phe Cys Glu Gly Ser Thr Arg Thr Leu
193 225      230      235      240
195 Lys Leu Cys Asn Ser Gln Lys Cys Pro Arg Asp Ser Val Asp Phe Arg
196      245      250      255
198 Ala Ala Gln Cys Ala Glu His Asn Ser Arg Arg Phe Arg Gly Arg His
199      260      265      270
W--> 201 Tyr Lys Trp Lys Pro Tyr Thr Gln Val Glu Xaa Asp Leu Cys Lys Leu
202      275      280      285
204 Tyr Cys Ile Ala Glu Gly Phe Asp Phe Phe Phe Ser Leu Ser Asn Lys
205      290      295      300
207 Val Lys Asp Gly Thr Pro Cys Ser Glu Asp Ser Arg Asn Val Cys Ile
208 305      310      315      320
210 Asp Gly Ile Cys Glu Leu Ser Val Val Ser Thr Ser Ala His Met Pro
211      325      330      335
213 Gln Pro Pro Lys Glu Asp Leu Phe Ile Leu Pro Asp Glu Tyr Lys Ser
214      340      345      350
216 Cys Leu Arg His Lys Arg Ser Leu Leu Arg Ser His Arg Asn Glu Glu
217      355      360      365
219 Leu Asn Val Glu Thr Leu Val Val Val Asp Lys Lys Met Met Gln Asn
220      370      375      380
222 His Gly His Glu Asn Ile Thr Thr Tyr Val Leu Thr Ile Leu Asn Met
223 385      390      395      400
225 Val Ser Ala Leu Phe Lys Asp Gly Thr Ile Gly Gly Asn Ile Asn Ile
226      405      410      415
228 Ala Ile Val Gly Leu Ile Leu Leu Glu Asp Glu Gln Pro Gly Leu Val
229      420      425      430
231 Ile Ser His His Ala Asp His Thr Leu Ser Ser Phe Cys Gln Trp Gln
232      435      440      445
234 Ser Gly Leu Met Gly Lys Asp Gly Thr Arg His Asp His Ala Ile Leu
235      450      455      460
237 Leu Thr Gly Leu Asp Ile Cys Ser Trp Lys Asn Glu Pro Cys Asp Thr
238 465      470      475      480
240 Leu Gly Phe Ala Pro Ile Ser Gly Met Cys Ser Lys Tyr Arg Ser Cys
241      485      490      495
243 Thr Ile Asn Glu Asp Thr Gly Leu Gly Leu Ala Phe Thr Ile Ala His
244      500      505      510
246 Glu Ser Gly His Asn Phe Gly Met Ile His Asp Gly Glu Gly Asn Met
247      515      520      525
249 Cys Lys Lys Ser Glu Gly Asn Ile Met Ser Pro Thr Leu Ala Gly Arg
250      530      535      540
252 Asn Gly Val Phe Ser Trp Ser Pro Cys Ser Arg Gln Tyr Leu His Lys
253 545      550      555      560
255 Phe Leu Ser Thr Ala Gln Ala Ile Cys Leu Ala Asp Gln Pro Lys Pro
256      565      570      575
258 Val Lys Glu Tyr Lys Tyr Pro Glu Lys Leu Pro Gly Glu Leu Tyr Asp

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259				580					585					590			
261	Ala	Asn	Thr	Gln	Cys	Lys	Trp	Gln	Phe	Gly	Glu	Lys	Ala	Lys	Leu	Cys	
262				595				600					605				
264	Met	Leu	Asp	Phe	Lys	Lys	Asp	Ile	Cys	Lys	Ala	Leu	Trp	Cys	His	Arg	
265		610					615					620					
267	Ile	Gly	Arg	Lys	Cys	Glu	Thr	Lys	Phe	Met	Pro	Ala	Ala	Glu	Gly	Thr	
268	625					630					635					640	
270	Ile	Cys	Gly	His	Asp	Met	Trp	Cys	Arg	Gly	Gly	Gln	Cys	Val	Lys	Tyr	
271					645					650					655		
273	Gly	Asp	Glu	Gly	Pro	Lys	Pro	Thr	His	Gly	His	Trp	Ser	Asp	Trp	Ser	
274				660					665					670			
276	Ser	Trp	Ser	Pro	Cys	Ser	Arg	Thr	Cys	Gly	Gly	Gly	Val	Ser	His	Arg	
277			675					680					685				
279	Ser	Arg	Leu	Cys	Thr	Asn	Pro	Asn	Pro	Ser	His	Gly	Gly	Lys	Phe	Cys	
280		690					695					700					
282	Glu	Gly	Ser	Thr	Arg	Thr	Leu	Lys	Leu	Cys	Asn	Ser	Gln	Lys	Cys	Pro	
283	705					710					715					720	
285	Arg	Asp	Ser	Val	Asp	Phe	Arg	Ala	Ala	Gln	Cys	Ala	Glu	His	Asn	Ser	
286					725					730					735		
288	Arg	Arg	Phe	Arg	Gly	Arg	His	Tyr	Lys	Trp	Lys	Pro	Gln	Asp	Leu	Cys	
289				740					745				750				
291	Lys	Leu	Tyr	Cys	Ile	Ala	Glu	Gly	Phe	Asp	Phe	Phe	Phe	Ser	Leu	Ser	
292			755					760				765					
294	Asn	Lys	Val	Lys	Asp	Gly	Thr	Pro	Cys	Ser	Glu	Asp	Ser	Arg	Asn	Val	
295		770					775					780					
297	Cys	Ile	Asp	Gly	Ile	Cys	Glu	Xaa	Gly	Cys	Asp	Asn	Val	Leu	Gly	Ser	
298	785					790					795					800	
300	Asp	Ala	Val	Glu	Asp	Val	Cys	Gly	Val	Cys	Asn	Gly	Asn	Asn	Ser	Ala	
301					805					810					815		
303	Cys	Thr	Ile	His	Arg	Gly	Leu	Tyr	Thr	Lys	His	His	His	Thr	Asn	His	
304				820					825				830				
306	Tyr	His	Met	Val	Thr	Ile	Pro	Ser	Gly	Ala	Arg	Ser	Ile	Arg	Ile	Tyr	
307			835					840					845				
309	Glu	Met	Asn	Val	Ser	Thr	Ser	Tyr	Ile	Ser	Val	Arg	Asn	Ala	Leu	Arg	
310		850					855					860					
312	Arg	Tyr	Tyr	Leu	Asn	Gly	His	Trp	Thr	Val	Asp	Trp	Pro	Gly	Arg	Tyr	
313	865					870					875					880	
315	Lys	Phe	Ser	Gly	Thr	Thr	Phe	Asp	Tyr	Arg	Arg	Ser	Tyr	Asn	Glu	Pro	
316					885					890					895		
318	Glu	Asn	Leu	Ile	Ala	Thr	Gly	Pro	Thr	Asn	Glu	Thr	Leu	Ile	Val	Glu	
319				900					905				910				
321	Leu	Leu	Phe	Gln	Gly	Arg	Asn	Pro	Gly	Val	Ala	Trp	Glu	Tyr	Ser	Met	
322			915					920					925				
324	Pro	Arg	Leu	Gly	Thr	Glu	Lys	Gln	Pro	Pro	Ala	Gln	Pro	Ser	Tyr	Thr	
325		930					935					940					
327	Trp	Ala	Ile	Val	Arg	Ser	Glu	Cys	Ser	Val	Ser	Cys	Gly	Gly	Gly	Arg	
328	945					950					955					960	
330	Cys	Leu	Pro	Val	Leu	Leu	Leu	Glu	Ala	Ala	Cys	Gln	Pro	Ser	Ala	Thr	
331					965				970						975		

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 857, 858, 2383, 2983

Seq#:2; Xaa Pos. 283, 792

Seq#:23; N Pos. 2196, 2230, 2261, 2270, 2295, 2301

Seq#:34; Xaa Pos. 450

Seq#:65; Xaa Pos. 41

VERIFICATION SUMMARY

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L:96 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:840
M:341 Repeated in SeqNo=1
L:201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:272
M:341 Repeated in SeqNo=2
L:1956 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:2160
M:341 Repeated in SeqNo=23
L:3356 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:448
L:6506 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:65 after pos.:32